

C. L. autman

1646

#3

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/339,153A

DATE: 09/10/1999
TIME: 15:09:44

INPUT SET: S33278.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Lok, Si
6 Adams, Robyn L.
7 Jelmsberg, Anna C.
8 Whitmore, Theodore E.
9 Farrah, Theresa M.
10
11 (ii) TITLE OF THE INVENTION: MAMMALIAN ZCYTOR11
12
13
14 (iii) NUMBER OF SEQUENCES: 6
15
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Zymogenetics
18 (B) STREET: 1201 Eastlake Ave East
19 (C) CITY: Seattle
20 (D) STATE: WA
21 (E) COUNTRY: USA
22 (F) ZIP: 98102
23
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Diskette
26 (B) COMPUTER: IBM Compatible
27 (C) OPERATING SYSTEM: DOS
28 (D) SOFTWARE: FastSEQ for Windows Version 2.0
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER:
32 (B) FILING DATE:
33 (C) CLASSIFICATION:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER:
37 (B) FILING DATE:
38
39
40
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: Lunn, Paul G
43 (B) REGISTRATION NUMBER: 32,743
44 (C) REFERENCE/DOCKET NUMBER: 97-52
45
46 (ix) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: 206-442-6627
48 (B) TELEFAX: 206-442-6678
49 (C) TELEX:

50

51

52 (2) INFORMATION FOR SEQ ID NO:1:

53

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 2831 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

59

60 (ii) MOLECULE TYPE: cDNA

61 (ix) FEATURE:

62

63 (A) NAME/KEY: Coding Sequence

64 (B) LOCATION: 34...1755

65 (D) OTHER INFORMATION:

66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

68

69 TAGAGGCCAA GGGAGGGCTC TGTGCCAGCC CCG ATG AGG ACG CTG CTG ACC ATC 54

70 Met Arg Thr Leu Leu Thr Ile

71 1 5

72

73 TTG ACT GTG GGA TCC CTG GCT GCT CAC GCC CCT GAG GAC CCC TCG GAT 102

74 Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp

75 10 15 20

76

77 CTG CTC CAG CAC GTG AAA TTC CAG TCC AGC AAC TTT GAA AAC ATC CTG 150

78 Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

79 25 30 35

80

81 ACG TGG GAC AGC GGG CCA GAG GGC ACC CCA GAC ACG GTC TAC AGC ATC 198

82 Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile

83 40 45 50 55

84

85 GAG TAT AAG ACG TAC GGA GAG AGG GAC TGG GTG GCA AAG AAG GGC TGT 246

86 Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys

87 60 65 70

88

89 CAG CGG ATC ACC CGG AAG TCC TGC AAC CTG ACG GTG GAG ACG GGC AAC 294

90 Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn

91 75 80 85

92

93 CTC ACG GAG CTC TAC TAT GCC AGG GTC ACC GCT GTC AGT GCG GGA GGC 342

94 Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly

95 90 95 100

96

97 CGG TCA GCC ACC AAG ATG ACT GAC AGG TTC AGC TCT CTG CAG CAC ACT 390

98 Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr

99 105 110 115

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100																		
101	ACC	CTC	AAG	CCA	CCT	GAT	GTG	ACC	TGT	ATC	TCC	AAA	GTG	AGA	TCG	ATT		438
102	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile		
103	120					125					130					135		
104																		
105	CAG	ATG	ATT	GTT	CAT	CCT	ACC	CCC	ACG	CCA	ATC	CGT	GCA	GGC	GAT	GGC		486
106	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly		
107					140						145				150			
108																		
109	CAC	CGG	CTA	ACC	CTG	GAA	GAC	ATC	TTC	CAT	GAC	CTG	TTC	TAC	CAC	TTA		534
110	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu		
111				155					160					165				
112																		
113	GAG	CTC	CAG	GTC	AAC	CGC	ACC	TAC	CAA	ATG	CAC	CTT	GGA	GGG	AAG	CAG		582
114	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln		
115			170					175					180					
116																		
117	AGA	GAA	TAT	GAG	TTC	TTC	GGC	CTG	ACC	CCT	GAC	ACA	GAG	TTC	CTT	GGC		630
118	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly		
119		185					190					195						
120																		
121	ACC	ATC	ATG	ATT	TGC	GTT	CCC	ACC	TGG	GCC	AAG	GAG	AGT	GCC	CCC	TAC		678
122	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr		
123	200					205					210					215		
124																		
125	ATG	TGC	CGA	GTG	AAG	ACA	CTG	CCA	GAC	CGG	ACA	TGG	ACC	TAC	TCC	TTC		726
126	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe		
127					220					225					230			
128																		
129	TCC	GGA	GCC	TTC	CTG	TTC	TCC	ATG	GGC	TTC	CTC	GTC	GCA	GTA	CTC	TGC		774
130	Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys		
131				235					240					245				
132																		
133																		
134	TAC	CTG	AGC	TAC	AGA	TAT	GTC	ACC	AAG	CCG	CCT	GCA	CCT	CCC	AAC	TCC		822
135	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser		
136			250					255					260					
137																		
138	CTG	AAC	GTC	CAG	CGA	GTC	CTG											

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153																		
154	GGG	CAG	CCA	GAC	ATC	TCC	ATC	CTC	CAG	CCC	TCC	AAC	GTG	CCA	CCT	CCC		1062
155	Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln	Pro	Ser	Asn	Val	Pro	Pro	Pro		
156			330					335					340					
157																		
158	CAG	ATC	CTC	TCC	CCA	CTG	TCC	TAT	GCC	CCA	AAC	GCT	GCC	CCT	GAG	GTC		1110
159	Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala	Pro	Asn	Ala	Ala	Pro	Glu	Val		
160		345					350					355						
161																		
162	GGG	CCC	CCA	TCC	TAT	GCA	CCT	CAG	GTG	ACC	CCC	GAA	GCT	CAA	TTC	CCA		1158
163	Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val	Thr	Pro	Glu	Ala	Gln	Phe	Pro		
164	360					365					370					375		
165																		
166	TTC	TAC	GCC	CCA	CAG	GCC	ATC	TCT	AAG	GTC	CAG	CCT	TCC	TCC	TAT	GCC		1206
167	Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	Val	Gln	Pro	Ser	Ser	Tyr	Ala		
168					380					385					390			
169																		
170	CCT	CAA	GCC	ACT	CCG	GAC	AGC	TGG	CCT	CCC	TCC	TAT	GGG	GTA	TGC	ATG		1254
171	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro	Pro	Ser	Tyr	Gly	Val	Cys	Met		
172				395				400						405				
173																		
174	GAA	GGT	TCT	GGC	AAA	GAC	TCC	CCC	ACT	GGG	ACA	CTT	TCT	AGT	CCT	AAA		1302
175	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	Gly	Thr	Leu	Ser	Ser	Pro	Lys		
176			410					415					420					
177																		
178																		
179	CAC	CTT	AGG	CCT	AAA	GGT	CAG	CTT	CAG	AAA	GAG	CCA	CCA	GCT	GGA	AGC		1350
180	His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln	Lys	Glu	Pro	Pro	Ala	Gly	Ser		
181		425					430					435						
182																		
183	TGC	ATG	TTA	GGT	GGC	CTT	TCT	CTG	CAG	GAG	GTG	ACC	TCC	TTG	GCT	ATG		1398
184	Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln	Glu	Val	Thr	Ser	Leu	Ala	Met		
185	440					445					450					455		
186																		
187	GAG	GAA	TCC	CAA	GAA	GCA	AAA	TCA	TTG	CAC	CAG	CCC	CTG	GGG	ATT	TGC		1446
188	Glu	Glu	Ser	Gln	Glu	Ala	Lys	Ser	Leu	His	Gln	Pro	Leu	Gly	Ile	Cys		
189					460					465					470			
190																		
191	ACA	GAC	AGA	ACA	TCT	GAC	CCA	AAT	GTG	CTA	CAC	AGT	GGG	GAG				

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206
207   CTT GTG TGT CCC AAG GAT GAA GCC AAG AGC CCA GCC CCT GAG ACC TCA      1686
208   Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
209               540                      545                      550
210
211   GAC CTG GAG CAG CCC ACA GAA CTG GAT TCT CTT TTC AGA GGC CTG GCC      1734
212   Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
213               555                      560                      565
214
215   CTG ACT GTG CAG TGG GAG TCC TGAGGGGAAT GGGAAAGGCT TGGTGCTTCC TCCC      1789
216   Leu Thr Val Gln Trp Glu Ser
217               570
218
219   TGTCCCTACC CAGTGTACACA TCCTTGGCTG TCAATCCCAT GCCTGCCCCAT GCCACACACT      1849
220   CTGCGATCTG GCCTCAGACG GGTGCCCTTG AGAGAAGCAG AGGGAGTGCG ATGCAGGGCC      1909
221   CCTGCCATGG GTGCGCTCCT CACCGGAACA AAGCAGCATG ATAAGGACTG CAGCGGGGGA      1969
222   GCTCTGGGGA GCAGCTTGTG TAGACAAGCG CGTGCTCGCT GAGCCCTGCA AGGCAGAAAT      2029
223   GACAGTGCAA GGAGGAAATG CAGGGAAACT CCGGAGGTCC AGAGCCCCAC CTCCTAACAC      2089
224   CATGGATTCA AAGTGCTCAG GGAATTTGCC TCTCCTTGCC CCATTCTTGG CCAGTTTCAC      2149
225   AATCTAGCTC GACAGAGCAT GAGGCCCTG CCTCTTCTGT CATTGTTCAA AGGTGGGAAG      2209
226   AGAGCCTGGA AAAGAACCAG GCCTGGA AAA GAACCAGAAG GAGGCTGGGC AGAACCAGAA      2269
227   CAACCTGCAC TTCTGCCAAG GCCAGGGCCA GCAGGACGGC AGGACTCTAG GGAGGGGTGT      2329
228   GGCCTGCAGC TCATTCCCAG CCAGGGCAAC TGCCTGACGT TGCACGATTT CAGCTTCATT      2389
229   CCTCTGATAG AACAAAGCGA AATGCAGGTC CACCAGGGAG GGAGACACAC AAGCCTTTTC      2449
230   TGCAGGCAGG AGTTTCAGAC CCTATCCTGA GAATGGGGTT TGAAAGGAAG GTGAGGGCTG      2509
231   TGGCCCCCTGG ACGGGTACAA TAACACACTG TACTGATGTC ACAACTTTGC AAGCTCTGCC      2569
232   TTGGGTTTCTG CCCATCTGGG CTCAAATTCC AGCCTCACCA CTCACAAGCT GTGTGACTTC      2629
233   AAACAAATGA AATCAGTGCC CAGAACCTCG GTTTCCTCAT CTGTAATGTG GGGATCATAA      2689
234   CACCTACCTC ATGGAGTTGT GGTGAAGATG AAATGAAGTC ATGTCTTTAA AGTGCTTAAT      2749
235   AGTGCCTGGT ACATGGGCAG TGCCCAATAA ACGGTAGCTA TTTAAAAAAA AAAAAAAAAA      2809
236   AAAAAAATAG CGGCCGCCTC GA                                     2831

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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250
251   Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
252       1             5             10             15
253   Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
254               20             25             30
255   Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
256               35             40             45
257   Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
258       50             55             60

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SEQUENCE VERIFICATION REPORT
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